NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

	1.	This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
4	2.	This application does not contain, as a separate part of the disclosure on paper copy, a 'Sequence Listing' as required by 37 C.F.R. 1.821(c).
	3.	A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
	4.	A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not edimply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
	5.	The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
	ŝ.	The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
	7.	Other:
Αģ	plic	cant Must Provide:
Ø	Aπ	initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
	An ent	initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its ry into the specification.
$ \sqrt{} $	app	statement that the content of the paper and computer readable copies are the same and, where blicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 325(b) or 1.825(d).
For	qu	estions regarding compliance to these requirements, please contact:
For	Ru	iles Interpretation, call (703) 308-4216
For	CF	RF Submission Help, call (703) 308-4212
ror	78	itentin software help, call (703) 308-6856

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/027,777B

DATE: 06/07/1999 TIME: 12:17:23

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This Raw Listing contains the General Information Section and up to the first 5 pages.

1			SEQUENCE LISTING	
2		.		CAITES
3 4	(1) General In	formation:		ENTERED
5 6 7 8	(i) APPLIC	ANT: IMMER, Han FORSSMANN, ADERMANN, KLESSEN, C	Wolf-Georg Knut	
9				
10 11	(ii) TITLE	OF INVENTION: P	ROCESS AND INTERMINATE AND HIGHLY DIS	EDIATE PRODUCTS FOR RIFIED CARDIODILATIN
. 12	FRAGMENTS	ODIDATIN PRAGME	NIS AND HIGHDI TO	
13				
14	(iii) NUMBER	OF SEQUENCES:	11	
15 16	/in coppe	PONDENCE ADDRES	c.	
17			do, Marmelstein, 1	Murrav & Oram
18			eenth Street, N.W	
19	· ,	ITY: Washington		
20	• •	TATE: D.C.		•
21 22	, ,	OUNTRY: USA IP: 20005-4810		
23	(F) Z	IP. 20005-4010		
24	(V) COMPUT	ER READABLE FOR	M:	
25		EDIUM TYPE: Flo		
26		OMPUTER: IBM PC		
27 28			: PC-DOS/MS-DOS In Release #1.0,	Version #1 30
26 29	(D) S	OFIWARE: Patent	In Release #1.0,	version #1.50
30	(vi) CURREN	T APPLICATION D	ATA:	
31			ER: US 09/027,777	
32	` '	'ILING DATE: 23-	FEB-1998	
33	(c) c	LASSIFICATION:		
34 35	(vii) PRTOR	APPLICATION DAT	Ά:	
36			ER: DE 44 20 381.	0
37		'ILING DATE: 02-		
38				
39	•	APPLICATION DAT		
40 41	, ,	PPLICATION NUMB	ER: DE 195 13 784	. 1
41	(B) E	ILING DATE: 10-	AFR-1993	
43	(viii) ATTORN	EY/AGENT INFORM	ATION:	
44		NAME: Kitts, Mon		
45		REGISTRATION NUM		
46	(C) F	EFERENCE/DOCKET	NUMBER: P1614-80	19

RAW SEQUENCE LISTING PATENT APPLICATION US/09/027,777B

DATE: 06/07/1999 TIME: 12:17:24

47		
48		(ix) TELECOMMUNICATION INFORMATION:
49		(A) TELEPHONE: (202) 638-5000
50		(B) TELEFAX: (202) 368-4810
51		
52		
53	(2)	INFORMATION FOR SEQ ID NO:1:
54	\ - <i>\</i>	
55		(i) SEQUENCE CHARACTERISTICS:
56		(A) LENGTH: 17 amino acids
57		(B) TYPE: amino acid
58		(C) STRANDEDNESS:
59		(D) TOPOLOGY: linear
60		(2) 10102001. 111002
61		(ii) MOLECULE TYPE: peptide
62		(II) ModBook IIIE. peptide
63		
64		
65		(with GROUPING PROGRESSION, GROUP NO.1.
66		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
67		and the single sure between the single singl
68		Cys Phe Gly Gly Arg Met Asp Arg Ile Gly Ala Gln Ser Gly Leu Gly
69		1 5 10 15
70		
71		Cys
72		•
73		
74	(2)	INFORMATION FOR SEQ ID NO:2:
75		
76		(i) SEQUENCE CHARACTERISTICS:
77		(A) LENGTH: 15 amino acids
78		(B) TYPE: amino acid
79		(C) STRANDEDNESS:
80		(D) TOPOLOGY: linear
81		·
82		(ii) MOLECULE TYPE: peptide
83		
84		·
85		·
86		
87		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
88		
89		Leu Arg Ala Leu Leu Thr Ala Pro Arg Ser Leu Arg Arg Ser Ser
90		1 5 10 15
91		
92	(2)	INFORMATION FOR SEQ ID NO:3:
93	, - ,	
94		(i) SEQUENCE CHARACTERISTICS:
95		(A) LENGTH: 5 amino acids
96		(B) TYPE: amino acid
97		(C) STRANDEDNESS:
98		(D) TOPOLOGY: linear
99		(D) TOPOLOGI. IIIIedi
22		

RAW SEQUENCE LISTING PATENT APPLICATION US/09/027,777B

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		INPU1 SE1: 55215U.Tu
100	(ii)	MOLECULE TYPE: peptide
101		
102		
103		
104		
105	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:3:
106		
107	Asn	Ser Phe Arg Tyr
108	1	5
109		·
110	(2) INFO	RMATION FOR SEQ ID NO:4:
111		·
112	(i)	SEQUENCE CHARACTERISTICS:
113		(A) LENGTH: 37 amino acids
114		(B) TYPE: amino acid
115		(C) STRANDEDNESS:
116		(D) TOPOLOGY: linear
117		•
118	(ii)	MOLECULE TYPE: peptide
119	` '	• •
120		
121	(ix)	FEATURE:
122	νγ	(A) NAME/KEY: Peptide
123		(B) LOCATION: 115
124		(D) OTHER INFORMATION: /note= "Xaa chain is an amino acid
125	chain of	0 - 15 amino acids."
126	· · · · · · · · · · · · · · · · · · ·	25 dilizito dozdavi
127	(ix)	FEATURE:
128	(=,	(A) NAME/KEY: Peptide
129		(B) LOCATION: 3337
130		(D) OTHER INFORMATION: /note= "Xaa chain is an amino acid
131	chain of	0 - 5 amino acids."
132	Chain Oi	J dimino dolds.
133	/iv\	FEATURE:
134	(17)	(A) NAME/KEY: Cross-links
135		(B) LOCATION: 1632
136		(b) Location. 10::32
137		
137	/vi\	SEQUENCE DESCRIPTION: SEQ ID NO:4:
139	(XI)	SEQUENCE DESCRIPTION. SEQ ID NO.4.
140	Vaa	Van
		Xaa
141	1	5 10 15
142	Dho	Clu Clu Ame Not Acm Ame The Clu Ale Clu Cor Clu Lou Clu Cuc
143	Pne	Gly Gly Arg Met Asp Arg Ile Gly Ala Gln Ser Gly Leu Gly Cys
144		20 25 30
145	W	Vac Vac Vac
146	хаа	Xaa Xaa Xaa
147		35
148		DUNGUAN DAD GEO ED NO E
149	(2) INFO	RMATION FOR SEQ ID NO:5:
150		
151	(i)	SEQUENCE CHARACTERISTICS:
152	•	(A) LENGTH: 32 amino acids

RAW SEQUENCE LISTING PATENT APPLICATION US/09/027,777B

DATE: 06/07/1999 TIME: 12:17:24

	INPUT SET: S32130.raw
153	(B) TYPE: amino acid
154	(C) STRANDEDNESS:
155	(D) TOPOLOGY: linear
156	• /
157	(ii) MOLECULE TYPE: peptide
158	(11, mollocal trade popular
159	
160	(ix) FEATURE:
161	(A) NAME/KEY: Cross-links
162	(B) LOCATION: 1127
163	(B) LOCATION: 1127
164	() CECUENCE DECORPOTON, CEC ID NO.5.
165	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
166	The the Dee two Con Low the two Con Con Che Dhe Che Dry Nor Not
167	Thr Ala Pro Arg Ser Leu Arg Arg Ser Ser Cys Phe Gly Gly Arg Met
168	1 5 10 15
169	
170	Asp Arg Ile Gly Ala Gln Ser Gly Leu Gly Cys Asn Ser Phe Arg Tyr
171	20 25 30
172	
173	
174	(2) INFORMATION FOR SEQ ID NO:6:
175	
176	(i) SEQUENCE CHARACTERISTICS:
177	(A) LENGTH: 14 amino acids
178	(B) TYPE: amino acid
179	(C) STRANDEDNESS:
180	(D) TOPOLOGY: linear
181	
182	(ii) MOLECULE TYPE: peptide
183	
184	
185	(ix) FEATURE:
186	(A) NAME/KEY: Modified-site
187	(B) LOCATION: 1
188	(D) OTHER INFORMATION: /product= "Modified by a Boc protecting
189	group and a tBu protecting group"
190	
191	(ix) FEATURE:
192	(A) NAME/KEY: Modified-site
193	(B) LOCATION: 4
194	(D) OTHER INFORMATION: /note= "Modified by a tBu protecting
195	group and a Pbf protecting group"
196	good and a con process of good
197	(ix) FEATURE:
198	(A) NAME/KEY: Modified-site
199	(B) LOCATION: 7
200	(D) OTHER INFORMATION: /note= "Modified by a Pbf protecting
201	group"
201	Aronh
202	(ix) FEATURE:
203	(1x) FEATURE: (A) NAME/KEY: Modified-site
205	(B) LOCATION: 8

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	111 O 1 3E1. 332130.14W
206	(D) OTHER INFORMATION: /note= "Modified by a Pbf protecting
207	group"
208	3
209	(ix) FEATURE:
210	(A) NAME/KEY: Modified-site
211	(B) LOCATION: 9
212	(D) OTHER INFORMATION: /note= "Modified by a tBu protecting
213	group"
214	5r
	(in) PRAMIRE
215	(ix) FEATURE:
216	(A) NAME/KEY: Modified-site
217	(B) LOCATION: 10
218	(D) OTHER INFORMATION: /note= "Modified by a tBu protecting
219	group"
220	3.04p
	(day) DRAMINE.
221	(ix) FEATURE:
222	(A) NAME/KEY: Modified-site
223	(B) LOCATION: 11
224	(D) OTHER INFORMATION: /note= "Modified by a Acm protecting
225	group"
226	31-04P
227	
228	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
229	
230	Thr Ala Pro Arg Ser Leu Arg Arg Ser Ser Cys Phe Gly Gly
231	1 5 10
232	1
	AAN TURANYAMTAN DAN ARA TA WA Z.
233	(2) INFORMATION FOR SEQ ID NO:7:
233	(2) INFORMATION FOR SEQ ID NO:7: (i) SEQUENCE CHARACTERISTICS:
233 234	(i) SEQUENCE CHARACTERISTICS:
233 234 235 236	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids
233 234 235 236 237	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid
233 234 235 236 237 238	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS:
233 234 235 236 237 238 239	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid
233 234 235 236 237 238 239 240	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
233 234 235 236 237 238 239	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS:
233 234 235 236 237 238 239 240	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
233 234 235 236 237 238 239 240 241 242	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
233 234 235 236 237 238 239 240 241 242 243	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide
233 234 235 236 237 238 239 240 241 242 243	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE:
233 234 235 236 237 238 239 240 241 242 243 244	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site</pre>
233 234 235 236 237 238 239 240 241 242 243	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE:
233 234 235 236 237 238 239 240 241 242 243 244	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1</pre>
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1 (D) OTHER INFORMATION: /product= "Modified by a Fmoc</pre>
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1</pre>
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1 (D) OTHER INFORMATION: /product= "Modified by a Fmoc protecting group and a Pbf protecting group"</pre>
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1 (D) OTHER INFORMATION: /product= "Modified by a Fmoc protecting group and a Pbf protecting group" (ix) FEATURE:</pre>
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1 (D) OTHER INFORMATION: /product= "Modified by a Fmoc protecting group and a Pbf protecting group" (ix) FEATURE: (A) NAME/KEY: Modified-site</pre>
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1 (D) OTHER INFORMATION: /product= "Modified by a Fmoc protecting group and a Pbf protecting group" (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 3
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1 (D) OTHER INFORMATION: /product= "Modified by a Fmoc protecting group and a Pbf protecting group" (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 3
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1 (D) OTHER INFORMATION: /product= "Modified by a Fmoc protecting group and a Pbf protecting group" (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 3 (D) OTHER INFORMATION: /product= "Modified by a OtBu
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1 (D) OTHER INFORMATION: /product= "Modified by a Fmoc protecting group and a Pbf protecting group" (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 3
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255	<pre>(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1 (D) OTHER INFORMATION: /product= "Modified by a Fmoc protecting group and a Pbf protecting group" (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 3 (D) OTHER INFORMATION: /product= "Modified by a OtBu protecting group"</pre>
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1 (D) OTHER INFORMATION: /product= "Modified by a Fmoc protecting group and a Pbf protecting group" (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 3 (D) OTHER INFORMATION: /product= "Modified by a OtBu protecting group" (ix) FEATURE: (B) LOCATION: 3 (D) OTHER INFORMATION: /product= "Modified by a OtBu protecting group"
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257	(i) SEQUENCE CHARACTERISTICS:
233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 1 (D) OTHER INFORMATION: /product= "Modified by a Fmoc protecting group and a Pbf protecting group" (ix) FEATURE: (A) NAME/KEY: Modified-site (B) LOCATION: 3 (D) OTHER INFORMATION: /product= "Modified by a OtBu protecting group" (ix) FEATURE: (B) LOCATION: 3 (D) OTHER INFORMATION: /product= "Modified by a OtBu protecting group"



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